



SEQUENCE LISTING

<110> IMHOF, BEAT ALBET
AURRAND-LIONS, MICHEL

<120> VASCULAR ADHESION MOLECULES AND MODULATION OF THEIR
FUNCTION

<130> 11422/0264679

<140> 09/524,531

<141> 2000-03-13

<150> EP 99.200746.8

<151> 1999-03-11

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified_base

<222> (6)

<223> a, t, c, g, other or unknown

<220>

<221> modified base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 1

tayagntgyn nngcytcyaa

20

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> modified base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 2

taycrgtgyn nngcytcyaa

20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: primer

<220>

<221> modified base

<222> (10)..(12)

<223> a, t, c, g, other or unknown

<400> 3

taytaytgyn nngcytcyaa

20

<210> 4

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

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18

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

cgacaggtgt cagataaca

19

<210> 6

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

caccctcctc actcgt

16

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer used
for detection of JAM-2 transcript

<400> 7

gactcacaga caagtgac

18

<210> 8

<211> 16

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer used
for detection JAM-2 transcript

<400> 8
caccctcctc actcgt

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
Hprt cDNA

<400> 9
gttgataca ggccagactt tggtg

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
Hprt cDNA

<400> 10
gagggtaggc tggcctatag gct

<210> 11
<211> 1943
<212> DNA
<213> Mus musculus

<400> 11
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aatccagcaa ccgaaaccca gtggtacatg aatttgaaag tgtggaattg tcttgcatca 180
ttacggactc acagacaagt gaccctagga ttgaatggaa gaaaatccaa gatggccaaa 240
ccacatatgt gtattttgac aacaagattc aaggagacct ggcaggtcgc acagatgtgt 300
ttggaaaaaac ttccctgagg atctggaatg tgacacgacg ggattcagcc atctatcgct 360
gtgaggtcgt tgctctaaat gaccgaaaag aagttgatga gattaccatt gagttaattg 420
tgcaagtga ggcagtgacc cctgtctgca gaattccagc cgctgtacct gtaggcaaga 480
cggcaacact gcagtgccaa gagagcgagg gctatccccg gcctcactac agctggtacc 540
gcaatgatgt gccactgcct acagattcca gagccaatcc caggttccag aattcctctt 600
tccatgtgaa ctcgagaca ggcactctgg ttttcaatgc tgtccacaag gacgactctg 660
ggcagtacta ctgcattgct tccaatgacg caggtgcagc caggtgtgag gggcaggaca 720
tggaagtcta tgatttgaac attgctggga ttattggggg agtccttggt gtccttattg 780
ttcttgctgt gattacgatg ggcactctgt gtgcgtacag acgaggctgc ttcacagca 840
gtaaacaaga tggagaaagc tataagagcc caggggaagca tgacggtgtt aactacatcc 900
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cctttctggt ctccgttctc ccatgcaggg caatttgagc tgttttgcc ccaggctgtt 1260
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caacagcctg atgctgtgta cagtgcacca ggaagggttt caggcagtg cttgctccct 1380
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gaatgtgttt ggaatcagca ttttataaaa aaccctaaatc agaaagggtga aattgcttgc 1500

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25

23

tggaagagg	gctctgaccc	aggaaactct	ccttcccaag	agatgccagg	agataggaga	1560
acctgtctgt	cttaagtctg	aaatggtact	gaagtctcct	tttctattgg	tcttgcttat	1620
tttataaaaa	tttaacattc	taaattttgc	tagagatgta	ttttgattac	tgaaaatttc	1680
tatataaaact	gtaaataat	tgccatacag	tgtttcaaaa	cgtatttttt	tataatgagt	1740
tcaacttaag	gtagaaggct	tgggctgcta	gtgtttaatt	ggaaaatacc	agtagtaaa	1800
tcttttaagg	agttttctta	aggaggctgg	ctgaatattc	ccttgttcaa	aagaagtttt	1860
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aattccaatc	taaaaaaaaa	aaa				1943

<210> 12
 <211> 1631
 <212> DNA
 <213> Mus musculus

<400> 12						
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ccctcccctc	aaccctcttc	cacccttcaa	aagaaggact	gtccagacac	cacgtcctag	180
ggccagaaga	cctgccccca	cgacagtcgc	tggagacacc	ccagaccgga	gagactgaca	240
tcggggacagg	acccgcccct	ctgcttccac	ctctcaggga	cctcctctgc	tccgcccgcg	300
ggcgaagtgc	tgggagaccc	agccgcctgt	cgcgtcctg	cagggggacc	ctcagctagg	360
cagccagctg	gcgcccgcgt	agatggcgag	gagcccccaa	ggcctcctga	tgctgctgct	420
gctacactac	ttgatcgctg	ccctggacta	tcataaggca	aatgggtttt	ctgcatcaaa	480
agaccaccgt	caagaagtca	cagtaataga	gttccaagag	gctatttttg	cttgtaaaac	540
cccaaagaag	actacctcct	ccagactgga	gtggaagaag	gtgggacagg	gggtctcctt	600
ggtctactac	caacaggctc	tccaagggtga	ctttaaagac	cgtgctgaga	tgatagattt	660
caatatacga	atcaaaaatg	ttacaagaag	tgatgctgga	gagtatcgct	gtgaagtcag	720
cgctccgact	gagcaaggcc	agaacctgca	ggaagataaa	gtcatgctag	aagtactagt	780
ggctcctgct	gttctctgct	gtgaagtgcc	cacttctgtt	atgactggaa	gtgtggtgga	840
gctacgatgc	caggataaag	aaggaaaccc	agctccggag	tacatctggt	ttaaagatgg	900
cacaagtttg	ctagggaatc	caaaaggcgg	cacacacaac	aacagctcgt	acacaaatga	960
acacgaatct	ggaattctgc	aattcaacat	gatttccaag	atggacagtg	gagagtatta	1020
ctgcgaagcc	cgaactctg	tcggacaccg	caggtgcctt	gggaagcgaa	tgcaagtaga	1080
tgttctcaac	ataagcggca	tcatagcaac	ggttgtgggt	gtggccttcg	tgatttctgt	1140
atgtggcctt	ggcacatgct	atgctcagag	gaaaggctac	ttttcaaaa	aaacttctct	1200
ccagaagggc	agtcctgcat	ctaaagtcac	tacgatgggc	gaaaatgatt	tcaggcacac	1260
aaaatccttt	ataatttaaa	agaattccag	ttttgggctg	cccaaaacca	gttgtcacat	1320
gttattaaaa	tattgtaaaa	ctctgtgtct	tacacttgca	aagtgatgaa	gaaatatgaa	1380
agggaggttc	atcagaagtt	ttatgatctc	taactcacia	gaaatatttt	aagcaaaacg	1440
ttcttgccat	cactaaatta	caacctggca	tcttggtgtg	acctaaggga	aatgtctggt	1500
aatattctgg	tttttggaag	caaataaatg	tcagtttgga	gttgactata	tcacactgac	1560
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<210> 13
 <211> 310
 <212> PRT
 <213> Mus musculus

<400> 13															
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His	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Met	Ile	Glu	Ala	Val
			20					25						30	
Asn	Leu	Lys	Ser	Ser	Asn	Arg	Asn	Pro	Val	Val	His	Glu	Phe	Glu	Ser
		35					40					45			
Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	His	Ser	Gln	Thr	Ser	Asp	Pro	Arg
	50					55					60				
Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Gly	Gln	Thr	Thr	Tyr	Val	Tyr	Phe

50					55					60					
Lys 65	Lys	Val	Gly	Gln	Gly 70	Val	Ser	Leu	Val	Tyr 75	Tyr	Gln	Gln	Ala	Leu 80
Gln	Gly	Asp	Phe	Lys 85	Asp	Arg	Ala	Glu	Met 90	Ile	Asp	Phe	Asn	Ile 95	Arg
Ile	Lys	Asn	Val 100	Thr	Arg	Ser	Asp	Ala 105	Gly	Glu	Tyr	Arg	Cys 110	Glu	Val
Ser	Ala	Pro 115	Thr	Glu	Gln	Gly	Gln	Asn 120	Leu	Gln	Glu	Asp 125	Lys	Val	Met
Leu	Glu 130	Val	Leu	Val	Ala	Pro 135	Ala	Val	Pro	Ala	Cys 140	Glu	Val	Pro	Thr
Ser	Val	Met	Thr	Gly	Ser 150	Val	Val	Glu	Leu	Arg 155	Cys	Gln	Asp	Lys	Glu 160
Gly	Asn	Pro	Ala	Pro 165	Glu	Tyr	Ile	Trp	Phe 170	Lys	Asp	Gly	Thr	Ser 175	Leu
Leu	Gly	Asn 180	Pro	Lys	Gly	Gly	Thr	His 185	Asn	Asn	Ser	Ser	Tyr 190	Thr	Asn
Glu	His	Glu 195	Ser	Gly	Ile	Leu	Gln 200	Phe	Asn	Met	Ile	Ser 205	Lys	Met	Asp
Ser	Gly	Glu	Tyr	Tyr	Cys	Glu	Ala 215	Arg	Asn	Ser	Val 220	Gly	His	Arg	Arg
Cys	Pro	Gly	Lys	Arg	Met 230	Gln	Val	Asp	Val	Leu 235	Asn	Ile	Ser	Gly	Ile 240
Ile	Ala	Thr	Val	Val	Val	Val	Ala	Phe	Val 250	Ile	Ser	Val	Cys	Gly 255	Leu
Gly	Thr	Cys	Tyr 260	Ala	Gln	Arg	Lys	Gly 265	Tyr	Phe	Ser	Lys	Glu 270	Thr	Ser
Phe	Gln	Lys 275	Gly	Ser	Pro	Ala	Ser 280	Lys	Val	Thr	Thr	Met 285	Gly	Glu	Asn
Asp	Phe	Arg	His	Thr	Lys	Ser 295	Phe	Ile	Ile						

<210> 15
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 15
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 1 5 10 15
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 20 25 30
 Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu Phe Glu Ser
 35 40 45
 Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr Ser Asp Pro Arg

50					55					60					
Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	Thr	Tyr	Val	Phe	Phe
65					70					75					80
Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	Arg	Ala	Glu	Ile	Leu	Gly
				85					90					95	
Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	Thr	Arg	Arg	Asp	Ser	Ala	Leu
			100					105					110		
Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu
		115					120					125			
Ile	Val	Ile	Glu	Leu	Thr	Val	Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys
	130					135					140				
Arg	Val	Pro	Lys	Ala	Val	Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys
145						150				155					160
Gln	Glu	Ser	Glu	Gly	His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn
				165					170					175	
Asp	Val	Pro	Leu	Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn
			180					185					190		
Ser	Ser	Phe	His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala
		195					200					205			
Val	His	Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp
	210					215					220				
Ala	Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
225					230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val	Leu
				245					250					255	
Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly	Tyr	Phe
			260					265					270		
Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro	Gly	Lys	Pro
		275					280					285			
Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly	Asp	Phe	Arg	His
	290					295					300				
Lys	Ser	Ser	Phe	Val	Ile										
305					310										

<210> 16
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 16
 Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile Lys Asn Val Thr Arg
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 Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser Ala Pro Ala Glu Gln
 20 25 30
 Gly Gln Asn Leu Glu Asp Thr Val Thr Leu Glu Val Leu Val Ala Pro

35

40

45

Ala Val Pro Ser Cys Glu Val Pro Ser Ser Ala Leu Ser Gly Thr Val
50 55 60

Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala Pro Glu Tyr
65 70 75 80

Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro Arg Leu Gly
85 90 95

Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys Thr Gly Thr
100 105 110

Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly Glu Tyr Ser Cys
115 120 125

Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys Pro Gly Lys Arg Met
130 135 140

Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala Val Val Val
145 150 155 160

Val Ala Leu Val Ile Ser Val Cys Gly Leu Gly Val Cys Tyr Ala Gln
165 170 175

Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser Phe Gln Lys Ser Asn Ser
180 185 190

Ser Ser Lys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys His Thr Lys
195 200 205

Ser Phe Ile Ile
210

<210> 17

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 17

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ccagtgggtac	aggaatttga	aagtgtggaa	ctgtcttgca	tcattacgga	ttcgcagaca	180
agtgaaccca	ggatcgagt	gaagaaaatt	caagatgaac	aaaccacata	tgtgtttttt	240
gacaacaaaa	ttcagggaga	cttgccgggt	cgtgcagaaa	tactggggaa	gacatccctg	300
aagatctgga	atgtgacacg	gagagactca	gccctttatc	gctgtgaggt	cgttgctcga	360
aatgaccgca	aggaaattga	tgagattgtg	atcgagttaa	ctgtgcaagt	gaagccagt	420
acccctgtct	gtagagtgcc	gaaggctgta	ccagtaggca	agatggcaac	actgcactgc	480
caggagagt	agggccaccc	ccggcctcac	tacagctggg	atcgcaatga	tgtaccactg	540
cccacggatt	ccagagccaa	tcccagattt	cgcaattctt	ctttccactt	aaactctgaa	600
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agttacaaga	accagatgga	accagatgga	gttaactaca	tccgcactga	cgaggagggc	900
gacttcagac	acaagtcac	gtttgtgatc	tgagaccggg	gtgtggctga	gagcgcacag	960
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tcgacagagc	tagacactct	tcaaagcttt	tcgtttggca	aggtgaccac	tactctttta	1080
ctctacaagc	ccatgaaaag	agaaattttc	tcaagaggac	ccggaaaatat	aaccccaagg	1140
aaccaaactg	gggtgcgttca	ctgaggtggg	gtccttaatt	tggttttggc	ctgattccca	1200
tgaaaataag	gggtctttta	gagtttggtg	cgtaaaacc	cccgccttggg	ccttggaacc	1260
cacatgttta	ccacctgcgt	taaaaaaaaa	aaaaaa			1296

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence
surrounding C-terminal cysteine of C2 domain
(endothelial cell line t-end)

<220>
<221> MOD_RES
<222> (4)
<223> Any amino acid

<400> 18
Tyr Arg Cys Xaa Ala Ser
1 5

<210> 19
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence
surrounding the C-terminal cysteine of C2 domain
(endothelial cell line t-end)

<220>
<221> MOD_RES
<222> (4)
<223> Any amino acid

<400> 19
Tyr Gln Cys Xaa Ala Ser
1 5

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence
surrounding the C-terminal cysteine of C2 domain
(endothelial cell line t-end)

<220>
<221> MOD_RES
<222> (4)
<223> Any amino acid

<400> 20
Tyr Tyr Cys Xaa Ala Ser
1 5

<210> 21
<211> 300
<212> PRT

<213> Mus musculus

<400> 21

Met Gly Thr Glu Gly Lys Ala Gly Arg Lys Leu Leu Phe Leu Phe Thr
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20 25 30
Ala Gln Ser Asp Val Gln Val Pro Glu Met Glu Ser Ile Lys Leu Thr
35 40 45
Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
50 55 60
Gln Gly Ser Thr Thr Ala Leu Val Cys Tyr Asn Ser Gln Ile Thr Ala
65 70 75 80
Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Glu Gly Ile Thr Phe Ser
85 90 95
Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu
100 105 110
Glu Gly Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu
115 120 125
Val Pro Pro Ser Lys Pro Thr Ile Ser Val Pro Ser Ser Val Thr Ile
130 135 140
Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
145 150 155 160
Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met Leu Thr Ala Asp
165 170 175
Ala Lys Lys Thr Arg Ala Phe His Asn Ser Ser Phe Thr Ile Asp Pro
180 185 190
Lys Ser Gly Asp Leu Tyr Phe Asp Phe Val Thr Ala Phe Asp Ser Gly
195 200 205
Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
210 215 220
Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
225 230 235 240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
245 250 255
Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
260 265 270
Thr Ala Pro Gly Lys Lys Val Ile Tyr Ser Gln Pro Ser Thr Arg Ser
275 280 285
Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295 300

<210> 22

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
surrounding the C-terminal cysteine of C2 domain
(endothelial cell line t-end)

<220>

<221> MOD_RES

<222> (2)

<223> Arg, Gln, Tyr, Ser

<220>

<221> MOD_RES

<222> (4)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (8)

<223> Any amino acid

<400> 22

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1 5